

Exhibit A

BLAST 2 SEQUENCES alignment of SEQ ID NO: 3 with 12ge20305orf30, a hypothetical H. pylori ORF disclosed by Smith et al. in WO 96/40893.



Blast 2 Sequences results

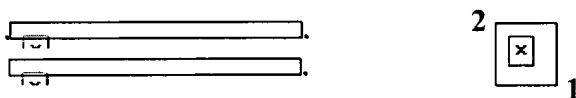
[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: ☒ Filter

Sequence 1 lcl|seq_1 Length 759 (1 .. 759)

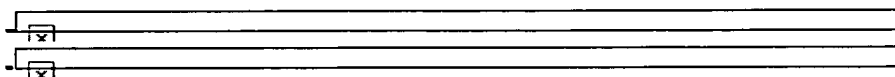
Sequence 2 lcl|seq_2 Length 768 (1 .. 768)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1344 bits (699), Expect = 0.0
Identities = 737/756 (97%)
Strand = Plus / Plus



Query: 1 atggcatacaaatatgatagagacttgggaatttttaaagcaattggaatctagtgattta
60
Sbjct: 10 atggcatacaaatatgatagagacttgggaatttttaaagcaactggaatctagtgattta
69

Query: 61 ttggatttggttgaggtgcttggttttggttaaagacggcgaaaaaagacacaatgaaaaa
120
Sbjct: 70 ttggatttggttcgaggtgcttggttttggttaaagacggcgaaaaaagacacaatgaaaaa
129

Query: 121 ctgaccagctccatagaatacaaaaaggcatggcgatgattacgctaaatacgcagaaaga
180

189

Query: 181 atcgctgaagagttgcaatactatgggagcaatagttttgcgagtttcattaaaggcgaa
240

Sbjct: 190 atcgctgaagagttgcaatactatgggagcaatagttttgcgagtttcattaaagggtgaa
 249

Query: 241 ggagtcttatatacaaagagattttatgcgatgtgtgcgataaattaaaggtcaattacaac
300

Sbjct: 250 ggagtcttatacaaagagattttatgcgatgtgtgcgataaattaaaggtcaattacaac
309

Query: 301 aagaaaactgaaacgactttaattgaacaaaacatgctttctaaaatcttagaaagaagt
360

369

Query: 361 ttggaagaaatggatgatgaagaagtgaagaaatgtgcatgaattatccataaaaaaac
420

429
Sbjct: 370 ctagaagaaatggatgatgaagaagtgaagaaatgtgcgatgaattgtccataaaaaaac

Query: 421 acggacaattttaaacagacaagccttaagcgcgggcgactttaacgctgtttaaaatgggg
480

489

Query: 481 ggtttttaaattcttatcaattagctgtcattggtgcgaatgcggtcgcaaaaaccattcta
540

549
Sbjct: 490 ggctttaaatcttatcaattagctgtcattggtgcgaatgcggttgcaaaaaccattcta

Query: 541 gggcgtggtttatcgcttgcgggcaatcagggtgcttacaagaactctgagctttttaaca
600

Sbjct: 550 gggcgtggtttatcgcttgcgggcaatcaagtgcttacaagaactctgagctttttaaca
 609

Query: 601 ggtcctgttggctggatcattacaggcgtatggacagcgattgatattgcagggccggct
660

|| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 610 ggccctgttggctggatcattacaggcgtatggacagcgattgatattgcagggccggct
669

Query: 661 tatagggttaaccataccggcatgcattgtggttgccactttacgcctaaaaacacagcaa
720

|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 670 tatagggttaaccataccggcatgcattgtggtcgcctttacgcctaaaaacgcaaca
729

Query: 721 gccaatggagataagaagtcggttgcaaatagaatcc 756

||||||| ||||||||||||||||||||||||||||
Sbjct: 730 gccaatgaagataagaagtcggttgcaaatagaatcc 765

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total
secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 166
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 759
Length of database: 12,305,973,192
Length adjustment: 26
Effective length of query: 733
Effective length of database: 12,305,973,166
Effective search space: 9020278330678
Effective search space used: 9020278330678
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)

CODING SEQUENCE WITH HOMOLOGY TO SEQ ID NO: 3 DISCLOSED BY
SMITH ET AL.

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN
RN 186778-60-9 REGISTRY
CN DNA (Helicobacter pylori strain J99 open reading frame
12ge20305orf30)
(9CI) (CA INDEX NAME)
FS NUCLEIC ACID SEQUENCE
SQL 768
NA 268 a 123 c 178 g 199 t
NTE doublestranded

SEQ 1 aggaataata tggcatacaa atatgataga gacttgggaat ttttaaagca
51 actggaatct agtgatttat tggatttggt cgagggtgctt gtttttggtta
101 aagacggcga aaaaagacac aatgaaaaac tcacaagctc catagaatac
151 aaaaggcatg gcgatgatta cgctaaatac gcagaaagaa tgcgtgaaga
201 gttgcaatac tatgggagca atagttttgc gagtttcatt aaagggtgaag
251 gagtcttata caaagagatt ttatgcatg tgtgcatgataa attaaagggtc
301 aattacaaca agaaaactga aacgacttta attgaacaaa acatgctttc
351 taaaatctta gaaagaagcc tagaagaaat ggatgatgaa gaagtgaag
401 aaatgtgcga tgaattgtcc ataaaaaaca cggacaattt gaacagacaa
451 gccttaagcg cggcgacttt aacgctgttt aaaatgggag gctttaaatc
501 ttatcaatta gctgtcattg ttgcgaatgc ggttgcaaaa accattctag
551 ggcgtgggtt atcgcttgcg ggcaatcaag tgcttacaag aactctgagc
601 tttttaacag gccctgttgg ctggatcatt acaggcggtat ggacagcgat
651 tgatattgca gggccggctt atagggtaac cataccggca tgcattgtgg
701 tcgccacttt acgcctaaaa acgcaacaag ccaatgaaga taagaagtgc
751 ttgcaaataa aatccggt

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological
study);

PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

HP30 Coding Sequence, SEQ ID NO: 3

atggcatacaaatatgatagagacttggaatttttaaagcaattggaatctagtgattta
ttggattttgtttgaggtgcttggttttggtaaagacggcgaaaaaagacacaatgaaaaa
ctgaccagctccatagaatacaaaaaggcatggcgatgattacgctaaatacgcagaaaga
atcgctgaagagttgcaatactatgggagcaatagttttgcgagtttcattaaaggcgaa
ggagtcttatatacaaagagattttatgcgatgtgtgcgataaattaaagggtcaattacaac
aagaaaactgaaacgactttaattgaacaaaacatgctttctaaaatcttagaaagaagt
ttggaagaaatggatgatgaagaagtgaagaaatgtgcgatgaattatccataaaaaac
acggacaatttaaacagacaagccttaagcgcggcgactttaacgctgtttaaaatgggg
ggttttaaatcttatcaattagctgtcattgttgcaatgcggtcgcaaaaaccattcta
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ggtcctgttggctggatcattacaggcgtatggacagcgattgatattgcagggccggct
tatagggttaaccataaccggcatgcattgtggttgccactttacgcctaaaaacacagcaa
gccaatggagataagaagtcggttgcaaatagaatccatt